REMARKS

Applicants submit herewith a Sequence Listing in paper and computer-readable form. Please enter this sequence listing into the specification of the above-captioned application.

These amendments are made to insert the sequence identifiers contained in the original sequence listing into the specification including Table 1, to make reference to each of the sequences disclosed in Figures 4, 7, 9 and 10 by use of a unique sequence identifier, and also to correct inadvertent typographical errors contained in the original Sequence Listing. Attorneys for Applicants were able to match the sequences provided in the originally submitted Sequence Listing with the sequences described in Table 1 by searching publicly available sequence databases, and have inserted the appropriate sequence identifiers. For example, Table 1 indicates that the clone designated "Old-1" is identified as vimentin; inputting all or a portion of the sequences provided in the original Sequence Listing as SEQ ID NO.:1 and doing a BLAST search against known genes identifies SEQ ID NO.:1 as vimentin; accordingly, Old-1 is matched with SEQ ID NO.:1. An alternative approach would be to search publicly available databases to find the sequence for vimentin and then match the retrieved sequence against those provided in the original Sequence Listing, which would result in recognizing SEQ ID NO.:1 as the sequence identifier for Old-1. One of ordinary skill in the art would have, at the time of the invention, been able to match the clones which had been identified as previously known genes with the sequences provided in the Sequence Listing, so that the addition of the identifiers to Table 1 in this amendment does not constitute new matter. With regard to novel genes listed in Table 1, the matching sequence identifiers could be deduced from either the text of the specification or the original claims, so that the addition of these identifiers to Table 1 does not constitute new matter.

In addition, the sequences present in the figures were compared with the sequences provided in the sequence listing and a number of errors were discovered. In particular:

(i) relative to the information provided in Figures 4A and B, SEQ. ID NO.:40 is missing a "ct" after the run of t's culminating at nt 336, and there is an extra "t" inserted into the sequence at nt 604;

(ii) similarly, SEQ. ID NO.:41 is missing an "a" after nt 153 and a "t" at nt 561 relative to the sequence provided in these same figures (4 A and B);

(iii) SEQ. ID NO.:43, the sequence of the *B. subtilis* PNPase displayed in Figures 10 A and B, is missing amino acid residues 19-58 relative to this figure;

(iv) SEQ. ID NO.:44, also derived from this same figure (10 A and B), is missing the alanine residue at position 173, but, apart from this error, this sequence is identical to that contained in SEQ. ID NO.:42, which was derived from Figure 4B; and

(v) one additional sequence has been added; as per the requirements of 37 C.F.R. § 1.821, SEQ. ID NO.:51 has been included to identify the human TNF AU-rich element depicted in Figure 7.

I hereby state that the content of the paper and computer readable copies of the Sequence Listing submitted in accordance with 37 C.F.R. §§ 1.821(c) and (e), respectively, are the same.

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted herewith in accordance with 37 C.F.R. § 1.82(f), does not include new matter.

Applicants believe a fee of $200.00 is due with this response for a two-month extension of time as required for a small entity under 37 C.F.R. §1.17(a)(2). A check in that amount is enclosed. The Commissioner is hereby authorized to charge payment of any additional fees

associated with this communication to Deposit Account No. 02-4377. Two copies of this paper are enclosed.

Respectfully submitted,

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Encl.

REPLACEMENT PARAGRAPHS SHOWING AMENDMENTS

The first full paragraph on page 9 at lines 19-14 is amended as follows:

Figure 4 (A-B) Sequence comparison between human and the mouse homologue of Old-35. Upper panel sequence of human Old-35 (h-Old-35; SEQ ID NO.: 40); Middle Panel: sequence of mouse Old-35 (m-Old-35; SEQ ID NO.: 41); and Lower panel: shared consensus sequences between human and mouse Old-35.

The paragraph beginning on page 9 at line 36 and bridging to page 10 at line 11 is amended as follows:

Figure 7 AU rich sequences found in the 3' untranslated region (UTR) of several lymphokine and protooncogene mRNAs. [Abbreviations] Abbreviations: Hu [-] = human, GM-CSF = granulocyte-monocyte colony stimulating factor ; IFN-α = interferon-α ; IL 2 = Interleukin 2 ; TNF = tumor necrosis factor; c-fos = fos proto-oncogene. The underlined/overlined AUUUA motif [if] of the largest sequence common to all mRNAs is shown. References: HuGM-CSF (SEQ ID NO.: 46) (Wong et al., 1985), Hu IFN-α (SEQ ID NO.: 47) (Goeddel et al., 1983), Hu IL 2 (SEQ ID NO.: 48) (Kashima et al., 1985), Hu TNF (SEQ ID NO.:51) (Nedwin et al., 1985), Hu c-fos (SEQ ID NO.:49) (van Straaten et al., 1983), Old 35 (SEQ ID NO.:50).

The last paragraph on page 10, lines 32-37, is amended as follows:

Figure 9 DNA sequence and predicted encoded protein of Old-35. (A) cDNA sequence of Old-35 (SEQ ID NO.:39). Alternate polyadenylation site is underlined. This site

is present in 10% of all cDNAs (Manley et al., 1988). (B) Predicted protein encoded by the Old-35 cDNA (SEQ ID NO.:42).

The first full paragraph on page 11, lines 1-11, is amended as follows:

Figure 10 Sequence similarity between the bacterial protein PNPase and the predicted protein sequence of Old-35. Upper panel: *Bacillus subtilis* PNPase sequence (SEQ ID NO.:43). Middle panel: predicted human Old-35 sequence (SEQ ID NO.:44). Lower panel: regions of consensus amino acids between the bacterial PNPase protein sequence and the predicted Old-35 protein sequence (SEQ ID NO.:45). Black boxed areas indicate [indicates] amino acid identity and gray boxed areas indicate amino acid similarities between the bacterial PNPase and the predicted Old-35 encoded protein.

The Table 1 at pages 38-40 is amended as follows:

TABLE 1

CLONE DESIGNATION	CLONE IDENTITY
Old-1 (SEQ ID NO.:1)	Vimentin
Old-2 (SEQ ID NO.:2)	Human ribosomal protein S3a, v-fos
Old-5 (SEQ ID NO.:3)	mRNA M phase phosphoprotein
Old-7 (SEQ ID NO.:4)	RIG-G, Cig49
Old-11 (SEQ ID NO.:5)	MHC class I lymphocyte antigen
Old-14 (SEQ ID NO.:6)	Human non-muscle myosin alkaline light chain
Old-18 (SEQ ID NO.:7)	Human ADP-ribosylation factor 4
Old-19 (SEQ ID NO.:8)	Human mitochondrial cytochrome oxidation
Old-24 (SEQ ID NO.:9)	56 kDa IFN inducible
Old-30 (SEQ ID NO.:10)	Ribosom[m]al protein L5
Old-32* (SEQ ID NO.:11)	Novel*
Old-34 (SEQ ID NO.:12)	IFN-inducible protein
Old-35* (SEQ ID NO.:40)	Novel*
Old-38 (SEQ ID NO.:13)	H.s. small acidic protein
Old-39 (SEQ ID NO.:14)	Human acidic ribosomal phosphatase
Old-42 (SEQ ID NO.:15)	Neurofibromatosis type 1
Old-59 (SEQ ID NO.:16)	Human nuclear receptor hTAK1
Old-60 (SEQ ID NO.:17)	Mitochondrial DNA
Old-61 (SEQ ID NO.:18)	Transcription factor I (99%)
Old-64* (SEQ ID NO.:19)	Novel*
Old-65 (SEQ ID NO.:20)	CDC16HS cell 81, 261-68
Old-74 (SEQ ID NO.:21)	Human ISG 54K gene (IFN-gamma)-cig42
Old-79 (SEQ ID NO.:22)	Human T-complex polypeptide I gene
Old-80 (SEQ ID NO.:23)	Vitamin D induced
Old-83* (SEQ ID NO.:24)	Novel*
Old-87* (SEQ ID NO.:25)	Novel*, Possibly similar to Old-83
Old-107* (SEQ ID NO.:26)	Novel*-Human homologue of Cow G-Protein
Old-113 (SEQ ID NO.:27)	DNA binding protein

Old-115 (SEQ ID NO.:28)	U1 small nuclear RNP
Old-119 (SEQ ID NO.:29)	Human HS1 protein
Old-121* (SEQ ID NO.:30)	Novel*
Old-137* (SEQ ID NO.:31)	Novel*
Old-139* (SEQ ID NO.:32)	Novel*
Old-140 (SEQ ID NO.:33)	Human putative trans. CA150
Old-142* (SEQ ID NO.:34)	Novel*
Old-144 (SEQ ID NO.:35)	MLN70 calcium-binding
Old-165 (SEQ ID NO.:36)	T-cell cyclophilin
Old-170 (SEQ ID NO.:37)	Human homologue of rat zinc transporter
Old-175 (5-3)* (SEQ ID NO.:38)	Novel*